

IN THE CLAIMS

1. (Currently amended) A computer system for screening nucleotide sequences, which comprises:

a target nucleotide sequence storing unit for storing target nucleotide sequence data;

a complementary sequence data storing unit for generating complementary sequence data from a probe nucleotide sequence ~~that may be bound to a target nucleotide sequence~~ and storing the complementary sequence data;

an evaluation processing unit for evaluating a binding possibility of the target nucleotide sequence data to the ~~complementary probe nucleotide~~ sequence data via a determination of whether the complementary sequence data of ~~the probe nucleotide sequence~~ is similar to a subsequence of the target nucleotide sequence data, ~~wherein the evaluation is performed~~ in descending order of edit distance of binding precision, ~~further~~ wherein edit distance is the number of times ~~nucleotide characters~~ ~~nucleotides~~ of the subsequence are required to be adjusted to generate the complementary sequence data, ~~and determining a binding possibility of the probe nucleotide sequence to the target nucleotide sequence; and~~

a storage unit for storing an evaluation result obtained by the evaluation processing unit for use by a user in determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence.

2. (Previously presented) The computer system according to claim 1, which further comprises a maximum edit distance storing unit for storing a maximum acceptable edit distance of binding precision between the target nucleotide sequence and the probe nucleotide sequence.

3. (Previously presented) The computer system according to claim 2, wherein the evaluation processing unit comprises a termination-determining unit for dynamically determining a termination point for the evaluation of the binding possibility, and the termination-determining unit determines whether the evaluation of the complementary sequence data is carried out over the maximum edit distance of binding precision.

4. (Withdrawn) A computer system for screening nucleotide sequences, which comprises:
a target nucleotide sequence storing unit for storing target nucleotide sequence data;
a complementary sequence data storing unit for generating complementary sequence data from a probe nucleotide sequence that may be bound to the target nucleotide sequence and storing the complementary sequence data;
an evaluation processing unit for designating a partial short chain sequence from said target nucleotide sequence data, as well as evaluating said complementary sequence data on the basis of every said partial sequence in descending order of edit distance, and determining the binding possibility of said probe nucleotide sequence to said target nucleotide sequence; and
a storage unit for storing the evaluation result obtained by said evaluation processing unit.

5. (Withdrawn) The computer system according to claim 4, which further comprises a maximum edit distance storing unit for storing a maximum acceptable edit distance between said target nucleotide sequence and said probe nucleotide sequence.

6. (Withdrawn) The computer system according to claim 5, wherein said evaluation processing unit comprises a termination-determining unit for dynamically determining termination of the evaluation, and said termination-determining unit determines whether the evaluation of said complementary sequence data is carried out over said maximum edit distance.

7. (Withdrawn) The computer system according to claim 5, wherein said evaluation processing unit, in response to the determination by said unit for dynamically determining termination of the evaluation, causes said partial sequence designating unit to designate another partial sequence having a predetermined overlap with the partial sequence most recently evaluated.

8. (Currently amended) A method for controlling a computer, which causes a computer system to execute screening of nucleotide sequences, the method causing a computer system to execute:

a step of storing target nucleotide sequence data and a probe nucleotide sequence;
a step of generating complementary sequence data from the probe nucleotide sequence that may be bound to a target nucleotide sequence and storing the complementary sequence data;
a step of storing a maximum acceptable edit distance of binding precision between the target nucleotide sequence and the probe nucleotide sequence;
a step of reading out the target nucleotide sequence data, the complementary sequence data and the maximum acceptable edit distance of binding precision from storing units of the target nucleotide sequence, the complementary sequence data and the maximum acceptable edit distance of binding precision, and evaluating a binding possibility of the target nucleotide sequence data to the complementary probe nucleotide sequence data via a determination of whether the complementary sequence data of the probe nucleotide sequence is similar to a subsequence of the target nucleotide sequence data, wherein the evaluation is performed in descending order of edit distance of binding precision, further wherein edit distance is the number of times nucleotide characters nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data; and
a step of storing a result of the evaluation in a storage unit for use by a user in determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence.

9. (Previously presented) The method for controlling a computer according to claim 8, wherein the reading out step further comprises:

a step of determining whether the evaluation of the complementary sequence data is carried out over the maximum edit distance of binding precision; and
a step of generating a termination signal in response to the determination result.

10. (Withdrawn) A method for controlling a computer, which causes a computer system to execute screening of nucleotide sequences, said method causing a computer system to execute:
a step of storing target nucleotide sequence data and a probe nucleotide sequence;

a step of generating complementary sequence data from a probe nucleotide sequence that may be bound to the target nucleotide sequence and storing the complementary sequence data;

a step of storing a maximum acceptable edit distance between said target nucleotide sequence and said probe nucleotide sequence;

a step of designating a partial short chain sequence from said target nucleotide sequence data, as well as evaluating said complementary sequence data on the basis of every said partial sequence in descending order of edit distance, and evaluating the binding possibility of said probe nucleotide sequence to said target nucleotide sequence; and

a step of storing the result of said evaluation in a storage unit.

11. (Withdrawn) The method for controlling a computer according to claim 10, wherein said evaluating step further comprises:

a step of determining whether the evaluation of said complementary sequence data is carried out over said maximum edit distance regarding at least one of said partial sequences; and

a step of dynamically terminating the evaluation in response to said determination result.

12. (Withdrawn) The method for controlling a computer according to claim 11, wherein said evaluating step further comprises:

a step of determining termination of the evaluation; and

a step of designating another partial sequence having a predetermined overlap with the partial sequence most recently evaluated, in response to the determination of said termination of the evaluation.

13. (Currently amended) A method for making a computer implemented process to enable screening of nucleotide sequences, the method comprising the steps of:

instantiating first computer instructions onto a computer readable medium, the first computer instructions configured to store target nucleotide sequence data and a probe nucleotide sequence;

instantiating second computer instructions onto a computer readable medium, the second computer instructions configured to generate complementary sequence data from the probe nucleotide sequence ~~that may be bound to a target nucleotide sequence~~ and storing the complementary sequence data;

instantiating third computer instructions onto a computer readable medium, the third computer instructions configured to store a maximum acceptable edit distance of binding precision between the target nucleotide sequence and the probe nucleotide sequence;

instantiating fourth computer instructions onto a computer readable medium, the fourth computer instructions configured to read out the target nucleotide sequence data, the complementary sequence data and the maximum acceptable edit distance of binding precision from each storing unit, and evaluating a binding possibility of the target nucleotide sequence data to the ~~complementary probe nucleotide~~ sequence data via a determination of whether the complementary sequence data ~~of the probe nucleotide sequence~~ is similar to a subsequence of the target nucleotide sequence data, wherein the evaluation is performed in descending order of edit distance of binding precision, further wherein edit distance is the number of times ~~nucleotide~~ characters nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data; and

instantiating fifth computer instructions onto a computer readable medium, the fifth computer instructions configured to store a result of the evaluation in a storage unit for use by a user in determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence.

14. (Previously presented) The method of claim 13, wherein the step of instantiating fourth computer instructions further comprises:

instantiating sixth computer instructions onto a computer readable medium, the sixth computer instructions configured to determine whether the evaluation of the complementary sequence data is carried out over the maximum edit distance of binding precision; and

instantiating seventh computer instructions onto a computer readable medium, the seventh computer instructions configured to terminate the evaluation in response to the determination result.

15. (Withdrawn) A computer executable program for a method for controlling a computer, which causes a computer system to execute screening of nucleotide sequences, said program controlling said computer system and causing the computer system to execute:

a step of storing target nucleotide sequence data and a probe nucleotide sequence;

a step of generating complementary sequence data from a probe nucleotide sequence that may be bound to the target nucleotide sequence and storing the complementary sequence data;

a step of storing a maximum acceptable edit distance between said target nucleotide sequence and said probe nucleotide sequence;

a step of designating a partial short chain sequence from said target nucleotide sequence data, as well as evaluating said complementary sequence data on the basis of every said partial sequence in descending order of edit distance, and evaluating the binding possibility of said probe nucleotide sequence to said target nucleotide sequence; and

a step of storing the result of said evaluation in a storage unit.

16. (Withdrawn) The computer executable program according to claim 15, wherein said evaluation step further comprises:

a step of determining whether the evaluation of said complementary sequence data is carried out over said maximum edit distance regarding at least one of said partial sequences;

a step of dynamically terminating the evaluation in response to said determination result; and

a step of designating another partial sequence having a predetermined overlap with the partial sequence most recently evaluated, in response to the determination of said termination of the evaluation.

17. (Currently amended) A computer-readable storage medium for recording a computer executable program for a computer control method, which causes a computer system to execute screening of nucleotide sequences, the program controlling the computer system and causing the computer system to execute:

- a step of storing target nucleotide sequence data and a probe nucleotide sequence;
- a step of generating complementary sequence data from a probe nucleotide sequence that may be bound to a target nucleotide sequence and storing the complementary sequence data;
- a step of storing a maximum acceptable edit distance of binding precision between the target nucleotide sequence and the probe nucleotide sequence;
- a step of reading out the target nucleotide sequence data, the complementary sequence data and the maximum acceptable edit distance of binding precision from each storing unit, and evaluating a binding possibility of the target nucleotide sequence data to the ~~complementary probe nucleotide sequence data~~ via a determination of whether the complementary sequence data of the probe nucleotide sequence is similar to a subsequence of the target nucleotide sequence data, wherein the evaluation is performed in descending order of edit distance of binding precision, further wherein edit distance is the number of times ~~nucleotide characters~~ nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data; and
- a step of storing a result of the evaluation in a storage unit for use by a user in determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence.

18. (Withdrawn) A computer-readable storage medium for recording a computer executable program for a method for controlling a computer, which causes a computer system to execute screening of nucleotide sequences, said program controlling said computer system and causing the computer system to execute:

- a step of storing target nucleotide sequence data and a probe nucleotide sequence;
- a step of generating complementary sequence data from a probe nucleotide sequence that may be bound to the target nucleotide sequence and storing the complementary sequence data;

a step of storing a maximum acceptable edit distance between said target nucleotide sequence and said probe nucleotide sequence;

a step of designating a partial short chain sequence from said target nucleotide sequence data, as well as evaluating said complementary sequence data on the basis of every said partial sequence in descending order of edit distance, and evaluating the binding possibility of said probe nucleotide sequence to said target nucleotide sequence; and

a step of storing the result of said evaluation in a storage unit.

19. (Withdrawn) A server on which screening of nucleotide sequences is executed through the network, said server comprising:

a database for storing target nucleotide sequence data;

a sending and receiving unit for receiving target designation data and a probe nucleotide sequence that may be bound to the target nucleotide sequence through the network, as well as sending the result of the screening through said network;

a complementary sequence data storing unit for generating complementary sequence data from said probe nucleotide sequence and storing the complementary sequence data; and

an evaluation processing unit for searching through said database using said target designation data, evaluating the searched target nucleotide sequence data and said complementary sequence data in descending order of edit distance, and determining the binding possibility of said probe nucleotide sequence to said target nucleotide sequence, as well as transmitting the result to said sending and receiving unit.